WE CLAIM:

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the ppgK gene, selected from the group consisting of

   a) a polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) a polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,

   c) a polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) a polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide according to claim 1, wherein the polypeptide has polyphosphate glucokinase activity.

3. The polynucleotide according to claim 1, wherein the polynucleotide is recombinant DNA which is capable of replication in coryneform bacteria.

4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.

5. The polynucleotide according to claim 3, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. The polynucleotide according to claim 3, wherein the DNA, comprises

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii).

7. The polynucleotide according to claim 6, further comprising

(iv) sense mutations of neutral function in (i).

8. The polynucleotide according to claim 6, wherein the hybridization of sequence (iii) is carried out under conditions of stringency corresponding at most to 2x SSC.

9. A polynucleotide sequence according to claim 1, wherein the polynucleotide codes for a polypeptide that comprises the amino acid sequence shown in SEQ ID NO: 2.

10. A coryneform bacteria in which the ppgK gene is enhanced, in particular over-expressed.

11. The coryneform bacteria, according to claim 10, wherein the ppgK gene is over-expressed.

12. A method for the fermentative preparation of L-amino acids in coryneform bacteria, comprising:

a) fermenting, in a medium, the coryneform bacteria which produce the desired L-amino acid and in which at least the ppgK gene or nucleotide sequences which code for it are enhanced.

13. The method according to claim 12, further comprising:

b) concentrating the L-amino acid in the medium or in the cells of the bacteria.

14. The method according to claim 13, further comprising:

c) isolating the L-amino acid.

15. The method according to claim 12, wherein the L amino acids are lysine.

16. The method according to claim 12, wherein ppgK gene or nucleotide sequences coding for this gene are overexpressed.

17. The method according to claim 12, wherein additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced in the bacteria.

18. The method according to claim 12, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

19. The method according to claim 12, wherein the bacteria are transformed with a plasmid vector and the plasmid vector carries the nucleotide sequence coding for the ppgK gene.

20. The method according to claim 12, wherein the expression of the polynucleotide(s) which code(s) for the ppgK gene is enhanced.

21. The method according to claim 20, wherein the expression of the polynucleotide(s) which code(s) for the ppgK gene is over-expressed.

22. The method according to claim 12, wherein the catalytic properties of the polypeptide for which the polynucleotide ppgK codes are increased.

23. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced or overexpressed; wherein the

one or more genes is/are selected from the group consisting of:

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,

the tpi gene which codes for triose phosphate isomerase,

the pgk gene which codes for 3-phosphoglycerate kinase,

the zwf gene which codes for glucose 6-phosphate dehydrogenase,

the pyc gene which codes for pyruvate carboxylase,

the mqo gene which codes for malate-quinone oxidoreductase,

the lysC gene which codes for a feed-back resistant aspartate kinase,

the lysE gene which codes for lysine export,

the hom gene which codes for homoserine dehydrogenase

the ilvA gene which codes for threonine dehydratase or the ilvA(Fbr) allele which codes for a feed back resistant threonine dehydratase,

the ilvBN gene which codes for acetohydroxy-acid synthase,

the ilvD gene which codes for dihydroxy-acid dehydratase, and

the zwa1 gene which codes for the Zwa1 protein.

24. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the genes are selected from the group consisting of:

the pck gene which codes for phosphoenol pyruvate carboxykinase,

the pgi gene which codes for glucose 6-phosphate isomerase,

the poxB gene which codes for pyruvate oxidase, and

the zwa2 gene which codes for the Zwa2 protein.

25. The method according to claim 12, wherein microorganisms of the species Corynebacterium glutamicum are employed.

26. A Coryneform bacteria comprising a vector which carries a polynucleotide according to claim 1.

27. A method for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes which code for polyphosphate glucokinase or have a high similarity with the sequence of the ppgK gene, comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.

28. The method according to claim 27, wherein arrays, micro arrays or DNA chips are used.